

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Goli, Surya K.

(ii) TITLE OF THE INVENTION: HUMAN LEA-MOTIF DEVELOPMENTAL PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0213 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Val Lys Tyr Phe Leu Gly Gln Ser Val Leu Arg Ser Ser Trp Asp
1 5 10 15
Gln Val Phe Ala Ala Phe Trp Gln Arg Tyr Pro Asn Pro Tyr Ser Lys
20 25 30

His Val Leu Thr Glu Asp Ile Val His Arg Glu Val Thr Pro Asp Gln
 35 40 45
 Lys Leu Leu Ser Arg Arg Leu Leu Thr Lys Thr Asn Arg Met Pro Arg
 50 55 60
 Trp Ala Glu Arg Leu Phe Pro Ala Asn Val Ala His Ser Val Tyr Val
 65 70 75 80
 Leu Glu Asp Ser Ile Val Asp Pro Gln Asn Gln Thr Met Thr Phe
 85 90 95
 Thr Trp Asn Ile Asn His Ala Arg Leu Met Val Val Glu Glu Arg Cys
 100 105 110
 Val Tyr Cys Val Asn Ser Asp Asn Ser Gly Trp Thr Glu Ile Arg Arg
 115 120 125
 Glu Ala Trp Val Ser Ser Ser Leu Phe Gly Val Ser Arg Ala Val Gln
 130 135 140
 Glu Phe Gly Leu Ala Arg Phe Lys Ser Asn Val Thr Lys Thr Met Lys
 145 150 155 160
 Gly Phe Glu Tyr Ile Leu Ala Lys Leu Gln Gly Glu Ala Pro Ser Lys
 165 170 175
 Thr Leu Val Glu Thr Ala Lys Glu Ala Lys Glu Lys Ala Lys Glu Thr
 180 185 190
 Ala Leu Ala Ala Thr Glu Lys Ala Lys Asp Leu Ala Ser Lys Ala Ala
 195 200 205
 Thr Lys Lys Gln Gln Gln Gln Gln Phe Val
 210 215

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GC GG TG GT GA	CT GAG CT ACG	AG C CT GG CG	CG GG TG GC	CG GAG C CCG	GC CC GG CCG	60
GCC CT CG CT	GC CT CC CAG	CT CC GAC CC	CT GAT GCT G	GC GG TG CT G	AG CC CG CT TC	120
GG CC GG GAC	AT GG TG AAG	AT TT CC TGG	CC AG AG CG	CT CC GG AG TT	CCT GGG AC CA	180
AG T GT T CG CC	GC CT T CT GG	AG CG GT A C C	GA AT CC CT AT	AG CAA AC AT G	TCT TG AC GG	240
AG AC AT AG TA	CA CC GG GAG	TG AC CC CT G	CC AG AA ACT G	CT GT CC CG GC	GA CT CC TG AC	300
CA AG AC CA AC	AG GA TG GCC AC	GCT GG GG CG	GCG ACT AT TT	CCT G CC AAT G	TT GCT CACT C	360
GG T GT AC GTC	CT GG AG GG ACT	CT AT TG GGA	CCC AC AG AA	CAG ACC AT G	CT AC CT TC AC	420
CT GG AA AC AT C	A ACC AC G C CC	GG CT GAT GGT	GG T GG AG GAA	CG AT GT GT TTT	ACT GT GT GAA	480
CT CT GAC AA AC	AG T GG CT GG A	CT GAA AT CCG	CC GGG AAG CC	TGG GT CT C CT	CT AG CT T ATT	540
TGG GT CT CC	AG AG CT GT CC	AG GA AT TT GG	TCT T GCC C G	TT CAA AA AG CA	AC GT GAC CAA	600
GACT AT GA AG	GG TT TT GA AT	AT AT CT TG G	TA AG CT G CAA	GG CG AG G C CC	CT TCC AAA AC	660
ACT T GT TG AG	AC AG CC AAG G	AAG CC AAG GA	GA AG G CAA AG	GAG AC GG CAC	TGG CAG CT AC	720
AG AG AAG G CC	AAG G AC CT CG	CC AG CA AG GC	GG CC AC CA AG	AAG CAG CAG C	AG CAG CA AC A	780
GT TT GT GT AG	CC AG T CT ACC	ACC ACC AC AG	CA CCC CAG AC	AG CT AG G CTT	AG CCC CT CT G	840
CC CT CC CT TC	ATT GT ACT					858

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank
(B) CLONE: 969170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Lys Tyr Cys Ala Ser Leu Gly Val Leu Lys Gly Pro Trp Asp
1 5 10 15
Gln Val Phe Ala Ala Phe Trp Gln Arg Tyr Pro Asn Pro Tyr Ser Lys
20 25 30
His Val Leu Thr Glu Asp Ile Val His Arg Glu Val Thr Ala Asp His
35 40 45
Lys Leu Leu Ser Arg Arg Leu Leu Thr Lys Thr Asn Arg Met Pro Arg
50 55 60
Trp Ala Glu Arg Phe Phe Pro Ala Asn Val Ala His Asn Val Tyr Ile
65 70 75 80
Val Glu Asp Ser Ile Val Asp Pro Lys Asn Arg Thr Met Thr Phe
85 90 95
Thr Trp Asn Ile Asn His Ala Arg Leu Met Ala Val Glu Glu Arg Cys
100 105 110
Val Tyr Arg Val Asn Pro Glu Asn Ser Ser Trp Thr Glu Val Lys Arg
115 120 125
Glu Ala Trp Val Ser Ser Ser Leu Phe Gly Val Ser Arg Ala Val Gln
130 135 140
Glu Phe Gly Leu Ala Arg Phe Lys Ser Asn Val Thr Lys Ser Thr Lys
145 150 155 160
Gly Phe Glu Tyr Val Leu Ala Arg Met Gln Gly Glu Ala Pro Ser Lys
165 170 175
Thr Leu Val Glu Thr Ala Lys Glu Ala Thr Glu Lys Ala Lys Glu Thr
180 185 190
Ala Leu Ala Ala Thr Glu Lys Ala Lys Asp Leu Ala Ser Lys Ala Ala
195 200 205
Thr Lys Lys Lys Gln Phe Val
210 215